

## **RAW SEQUENCE LISTING**

**The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.**

Application Serial Number: 10/630,518 A  
Source: JFW16  
Date Processed by STIC: 02/08/2006

**ENTERED**



IFW16

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/630,518A

DATE: 02/08/2006

TIME: 12:08:12

Input Set : A:\SEQ LIST 532792001100.txt  
 Output Set: N:\CRF4\02082006\J630518A.raw

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4 <110> APPLICANT: THE SALK INSTITUTE FOR BIOLOGICAL STUDIES
5   THE REGENTS OF THE UNIVERSITY OF CALIFORNIA
6   LILJEGREN, Sarah, Jean
7   ECKER, Joseph, R.
8   YANOFSKY, Martin, F.
10 <120> TITLE OF INVENTION: GENETIC CONTROL OF ORGAN ABSCISSION
13 <130> FILE REFERENCE: 532792001100
15 <140> CURRENT APPLICATION NUMBER: 10/630,518A
16 <141> CURRENT FILING DATE: 2003-07-29
18 <150> PRIOR APPLICATION NUMBER: US 60/264,974
19 <151> PRIOR FILING DATE: 2001-01-29
21 <150> PRIOR APPLICATION NUMBER: PCTUS02/01938
22 <151> PRIOR FILING DATE: 2002-01-22
24 <160> NUMBER OF SEQ ID NOS: 26
26 <170> SOFTWARE: FastSEQ for Windows Version 4.0
28 <210> SEQ ID NO: 1
29 <211> LENGTH: 1452
30 <212> TYPE: DNA
31 <213> ORGANISM: Arabidopsis thaliana
33 <220> FEATURE:
34 <221> NAME/KEY: CDS
35 <222> LOCATION: (1)...(1452)
37 <400> SEQUENCE: 1
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39 Met Asn Glu Lys Ala Asn Val Ser Lys Glu Leu Asn Ala Arg His Arg
40   1           5           10          15
42 aag att ctt gaa ggg ctt ctt aaa cat cca gag aac aga gaa tgt gct      96
43 Lys Ile Leu Glu Gly Leu Leu Lys His Pro Glu Asn Arg Glu Cys Ala
44   20          25           30
46 gac tgc aaa aca aaa ggt cca aga tgg gct agt gtt aat tta ggt atc    144
47 Asp Cys Lys Thr Lys Gly Pro Arg Trp Ala Ser Val Asn Leu Gly Ile
48   35          40           45
50 ttt atc tgc atg caa tgt tct ggg att cac agg agt ctc ggg gta cac    192
51 Phe Ile Cys Met Gln Cys Ser Gly Ile His Arg Ser Leu Gly Val His
52   50          55           60
54 ata tcg aag gtt cga tct gcc act ctg gac aca tgg ctc ccc gag cag    240
55 Ile Ser Lys Val Arg Ser Ala Thr Leu Asp Thr Trp Leu Pro Glu Gln
56   65          70           75          80
58 gtt gca ttt ata cag tca atg gga aat gat aaa gca aat agt tac tgg    288
59 Val Ala Phe Ile Gln Ser Met Gly Asn Asp Lys Ala Asn Ser Tyr Trp
60   85          90           95
62 gaa gca gag cta ccc cca aac tat gat aga gtt gga att gag aat ttt    336
63 Glu Ala Glu Leu Pro Pro Asn Tyr Asp Arg Val Gly Ile Glu Asn Phe

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64	100	105	110	
66	ata cgt gca aag tat gaa gag aag aga tgg gtt tct aga ggg gaa aag			384
67	Ile Arg Ala Lys Tyr Glu Glu Lys Arg Trp Val Ser Arg Gly Glu Lys			
68	115	120	125	
70	gct aga tca cct cct aga gtc gag cag gaa cgg cgg aaa tct gtg gag			432
71	Ala Arg Ser Pro Pro Arg Val Glu Gln Glu Arg Arg Lys Ser Val Glu			
72	130	135	140	
74	aga agt ggg ccg gga tat gag cat gga cat agt agt cct gta aat			480
75	Arg Ser Gly Pro Gly Tyr Glu His Gly His Ser Ser Ser Pro Val Asn			
76	145	150	155	160
78	ttg ttt gag gag agg aaa act att cca gca tct aga aca aga aat aat			528
79	Leu Phe Glu Glu Arg Lys Thr Ile Pro Ala Ser Arg Thr Arg Asn Asn			
80	165	170	175	
82	gtt gct gca acg aga ata aat ctt ccc gtg cct ccc caa gga ccc agt			576
83	Val Ala Ala Thr Arg Ile Asn Leu Pro Val Pro Pro Gln Gly Pro Ser			
84	180	185	190	
86	cag gtt ata aag cca cag cag aaa atg gag tct gca gct act cca gta			624
87	Gln Val Ile Lys Pro Gln Gln Lys Met Glu Ser Ala Ala Thr Pro Val			
88	195	200	205	
90	gag agg gag aaa caa gca gta aat gtt gca cca gca tca gat cct cca			672
91	Glu Arg Glu Lys Gln Ala Val Asn Val Ala Pro Ala Ser Asp Pro Pro			
92	210	215	220	
94	aag gtg gat ttt gct act gat ctg ttt aac atg cta tca atg gat gat			720
95	Lys Val Asp Phe Ala Thr Asp Leu Phe Asn Met Leu Ser Met Asp Asp			
96	225	230	235	240
98	tcg act aca aat acc tca gag gca act cct ggc gat act cct gcc gat			768
99	Ser Thr Thr Asn Thr Ser Glu Ala Thr Pro Gly Asp Thr Pro Ala Asp			
100	245	250	255	
102	gat aac tca tgg gct ggc ttt cag tct gct gga agt ggt caa acg gca			816
103	Asp Asn Ser Trp Ala Gly Phe Gln Ser Ala Gly Ser Gly Gln Thr Ala			
104	260	265	270	
106	gag aaa att gtc aca gcc aag cct gct gag agc agt tct cct cca gct			864
107	Glu Lys Ile Val Thr Ala Lys Pro Ala Glu Ser Ser Pro Pro Ala			
108	275	280	285	
110	tca tct tct gac ttt gag gat ttg ttt aag gac aca cct aat tta aca			912
111	Ser Ser Asp Phe Glu Asp Leu Phe Lys Asp Thr Pro Asn Leu Thr			
112	290	295	300	
114	act caa caa gca cca aaa gat gtg aaa ggc gat atc atg agc ctg ttt			960
115	Thr Gln Gln Ala Pro Lys Asp Val Lys Gly Asp Ile Met Ser Leu Phe			
116	305	310	315	320
118	gag aag acg aat ata gta tcg cct ttt gcc atg cat cag caa cag gtt			1008
119	Glu Lys Thr Asn Ile Val Ser Pro Phe Ala Met His Gln Gln Val			
120	325	330	335	
122	gct atg ctc gct cag cag caa gcc ctt tac atg gct gca gcg aaa gct			1056
123	Ala Met Leu Ala Gln Gln Ala Leu Tyr Met Ala Ala Ala Lys Ala			
124	340	345	350	
126	gct gga ggc act cca aac ggc gtg aat caa caa gct att gct aat gct			1104
127	Ala Gly Gly Thr Pro Asn Gly Val Asn Gln Gln Ala Ile Ala Asn Ala			
128	355	360	365	

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130	ctt	aac	gta	gct	tct	gca	aat	tgg	tca	aac	ccc	ggc	ggc	tac	cag	atc	1152
131	Leu	Asn	Val	Ala	Ser	Ala	Asn	Trp	Ser	Asn	Pro	Gly	Gly	Tyr	Gln	Ile	
132	370					375				380							
134	ccc	gga	atg	act	aac	ccc	gta	ggt	ggt	caa	gct	gat	ctc	cag	aaa	ctt	1200
135	Pro	Gly	Met	Thr	Asn	Pro	Val	Gly	Gly	Gln	Ala	Asp	Leu	Gln	Lys	Leu	
136	385					390				395				400			
138	atg	caa	aac	atg	aat	atg	aac	gca	aac	atg	aac	acg	aga	ccc	gca	caa	1248
139	Met	Gln	Asn	Met	Asn	Met	Asn	Ala	Asn	Met	Asn	Thr	Arg	Pro	Ala	Gln	
140						405				410				415			
142	ccg	caa	gag	aac	act	cta	caa	tac	cca	tca	tcc	agt	ttc	tac	aca	atg	1296
143	Pro	Gln	Glu	Asn	Thr	Leu	Gln	Tyr	Pro	Ser	Ser	Phe	Tyr	Thr	Met		
144						420				425				430			
146	ggt	caa	gct	aat	caa	gtg	aac	ggt	atg	acc	cca	aac	tca	acc	ggt	aaa	1344
147	Gly	Gln	Ala	Asn	Gln	Val	Asn	Gly	Met	Thr	Pro	Asn	Ser	Thr	Gly	Lys	
148						435				440				445			
150	cct	cag	tca	tca	tcc	gca	acc	caa	cca	aca	agc	acc	aca	cca	tct	tca	1392
151	Pro	Gln	Ser	Ser	Ser	Ala	Thr	Gln	Pro	Thr	Ser	Thr	Thr	Pro	Ser	Ser	
152						450				455				460			
154	caa	tca	ggc	aaa	gac	ttt	gat	ttc	tct	tcc	ttg	atg	gat	gga	atg	ttc	1440
155	Gln	Ser	Gly	Lys	Asp	Phe	Asp	Phe	Ser	Ser	Leu	Met	Asp	Gly	Met	Phe	
156						465				470				475			480
158	aca	aaa	cat	tga													1452
159	Thr	Lys	His	*													
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165	<212>	TYPE:	PRT														
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170	1					5				10					15		
171	Lys	Ile	Leu	Glu	Gly	Leu	Leu	Lys	His	Pro	Glu	Asn	Arg	Glu	Cys	Ala	
172						20				25					30		
173	Asp	Cys	Lys	Thr	Lys	Gly	Pro	Arg	Trp	Ala	Ser	Val	Asn	Leu	Gly	Ile	
174						35				40				45			
175	Phe	Ile	Cys	Met	Gln	Cys	Ser	Gly	Ile	His	Arg	Ser	Leu	Gly	Val	His	
176						50				55				60			
177	Ile	Ser	Lys	Val	Arg	Ser	Ala	Thr	Leu	Asp	Thr	Trp	Leu	Pro	Glu	Gln	
178						65				70				75			80
179	Val	Ala	Phe	Ile	Gln	Ser	Met	Gly	Asn	Asp	Lys	Ala	Asn	Ser	Tyr	Trp	
180						85				90				95			
181	Glu	Ala	Glu	Leu	Pro	Pro	Asn	Tyr	Asp	Arg	Val	Gly	Ile	Glu	Asn	Phe	
182						100				105				110			
183	Ile	Arg	Ala	Lys	Tyr	Glu	Glu	Lys	Arg	Trp	Val	Ser	Arg	Gly	Glu	Lys	
184						115				120				125			
185	Ala	Arg	Ser	Pro	Pro	Arg	Val	Glu	Gln	Glu	Arg	Arg	Lys	Ser	Val	Glu	
186						130				135				140			
187	Arg	Ser	Gly	Pro	Gly	Tyr	Glu	His	Gly	His	Ser	Ser	Ser	Pro	Val	Asn	
188						145				150				155			160
189	Leu	Phe	Glu	Glu	Arg	Lys	Thr	Ile	Pro	Ala	Ser	Arg	Thr	Arg	Asn	Asn	

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190	165	170	175
191	Val Ala Ala Thr Arg Ile Asn Leu Pro Val Pro Pro Gln Gly Pro Ser		
192	180	185	190
193	Gln Val Ile Lys Pro Gln Gln Lys Met Glu Ser Ala Ala Thr Pro Val		
194	195	200	205
195	Glu Arg Glu Lys Gln Ala Val Asn Val Ala Pro Ala Ser Asp Pro Pro		
196	210	215	220
197	Lys Val Asp Phe Ala Thr Asp Leu Phe Asn Met Leu Ser Met Asp Asp		
198	225	230	235
199	Ser Thr Thr Asn Thr Ser Glu Ala Thr Pro Gly Asp Thr Pro Ala Asp		
200	245	250	255
201	Asp Asn Ser Trp Ala Gly Phe Gln Ser Ala Gly Ser Gly Gln Thr Ala		
202	260	265	270
203	Glu Lys Ile Val Thr Ala Lys Pro Ala Glu Ser Ser Ser Pro Pro Ala		
204	275	280	285
205	Ser Ser Ser Asp Phe Glu Asp Leu Phe Lys Asp Thr Pro Asn Leu Thr		
206	290	295	300
207	Thr Gln Gln Ala Pro Lys Asp Val Lys Gly Asp Ile Met Ser Leu Phe		
208	305	310	315
209	Glu Lys Thr Asn Ile Val Ser Pro Phe Ala Met His Gln Gln Gln Val		
210	325	330	335
211	Ala Met Leu Ala Gln Gln Gln Ala Leu Tyr Met Ala Ala Ala Lys Ala		
212	340	345	350
213	Ala Gly Gly Thr Pro Asn Gly Val Asn Gln Gln Ala Ile Ala Asn Ala		
214	355	360	365
215	Leu Asn Val Ala Ser Ala Asn Trp Ser Asn Pro Gly Gly Tyr Gln Ile		
216	370	375	380
217	Pro Gly Met Thr Asn Pro Val Gly Gly Gln Ala Asp Leu Gln Lys Leu		
218	385	390	395
219	Met Gln Asn Met Asn Met Asn Ala Asn Met Asn Thr Arg Pro Ala Gln		
220	405	410	415
221	Pro Gln Glu Asn Thr Leu Gln Tyr Pro Ser Ser Ser Phe Tyr Thr Met		
222	420	425	430
223	Gly Gln Ala Asn Gln Val Asn Gly Met Thr Pro Asn Ser Thr Gly Lys		
224	435	440	445
225	Pro Gln Ser Ser Ser Ala Thr Gln Pro Thr Ser Thr Thr Pro Ser Ser		
226	450	455	460
227	Gln Ser Gly Lys Asp Phe Asp Phe Ser Ser Leu Met Asp Gly Met Phe		
228	465	470	475
229	Thr Lys His		480
233	<210> SEQ ID NO: 3		
234	<211> LENGTH: 1452		
235	<212> TYPE: DNA		
236	<213> ORGANISM: Arabidopsis thaliana		
238	<220> FEATURE:		
239	<221> NAME/KEY: CDS		
240	<222> LOCATION: (1)...(1452)		
242	<400> SEQUENCE: 3		
243	atg aac gag aaa gcc aac gtc tct aag gag ctt aat gcc cgc cat aga	48	

**RAW SEQUENCE LISTING**  
**PATENT APPLICATION: US/10/630,518A**

**DATE: 02/08/2006**  
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**Input Set : A:\SEQ LIST 532792001100.txt**  
**Output Set: N:\CRF4\02082006\J630518A.raw**

244	Met Asn Glu Lys Ala Asn Val Ser Lys Glu Leu Asn Ala Arg His Arg				
245	1	5	10	15	
247	aag att ctt qaa ggg ctt ctt aaa cat cca gag aac aga gaa tgt gct				96
248	Lys Ile Leu Glu Gly Leu Leu Lys His Pro Glu Asn Arg Glu Cys Ala				
249	20	25	30		
251	gac tgc aaa aca aaa ggt cca aga tgg gct agt gtt aat tta ggt atc				144
252	Asp Cys Lys Thr Lys Gly Pro Arg Trp Ala Ser Val Asn Leu Gly Ile				
253	35	40	45		
255	ttt atc tac atg caa tgt tct ggg att cac agg agt ctc ggg gta cac				192
256	Phe Ile Tyr Met Gln Cys Ser Gly Ile His Arg Ser Leu Gly Val His				
257	50	55	60		
259	ata tcg aag gtt cga tct gcc act ctg gac aca tgg ctc ccc gag cag				240
260	Ile Ser Lys Val Arg Ser Ala Thr Leu Asp Thr Trp Leu Pro Glu Gln				
261	65	70	75	80	
263	gtt gca ttt ata cag tca atg gga aat gat aaa gca aat agt tac tgg				288
264	Val Ala Phe Ile Gln Ser Met Gly Asn Asp Lys Ala Asn Ser Tyr Trp				
265	85	90	95		
267	gaa gca gag cta ccc cca aac tat gat aga gtt gga att gag aat ttt				336
268	Glu Ala Glu Leu Pro Pro Asn Tyr Asp Arg Val Gly Ile Glu Asn Phe				
269	100	105	110		
271	ata cgt gca aag tat gaa gag aag aga tgg gtt tct aga ggg gaa aag				384
272	Ile Arg Ala Lys Tyr Glu Glu Lys Arg Trp Val Ser Arg Gly Glu Lys				
273	115	120	125		
275	gct aga tca cct cct aga gtc gag cag gaa cg <sup>g</sup> cg <sup>g</sup> aaa tct gtg gag				432
276	Ala Arg Ser Pro Pro Arg Val Glu Gln Glu Arg Arg Lys Ser Val Glu				
277	130	135	140		
279	aga agt ggg cc <sup>g</sup> gga tat gag cat gga cat agt agt agt cct gta aat				480
280	Arg Ser Gly Pro Gly Tyr Glu His Gly His Ser Ser Ser Pro Val Asn				
281	145	150	155	160	
283	ttg ttt gag gag agg aaa act att cca gca tct aga aca aga aat aat				528
284	Leu Phe Glu Glu Arg Lys Thr Ile Pro Ala Ser Arg Thr Arg Asn Asn				
285	165	170	175		
287	gtt gct gca acg aga ata aat ctt ccc gtg cct ccc caa gga ccc agt				576
288	Val Ala Ala Thr Arg Ile Asn Leu Pro Val Pro Pro Gln Gly Pro Ser				
289	180	185	190		
291	cag gtt ata aag cca cag cag aaa atg gag tct gca gct act cca gta				624
292	Gln Val Ile Lys Pro Gln Gln Lys Met Glu Ser Ala Ala Thr Pro Val				
293	195	200	205		
295	gag agg gag aaa caa gca gta aat gtt gca cca gca tca gat cct cca				672
296	Glu Arg Glu Lys Gln Ala Val Asn Val Ala Pro Ala Ser Asp Pro Pro				
297	210	215	220		
299	aag gtg gat ttt gct act gat ctg ttt aac atg cta tca atg gat gat				720
300	Lys Val Asp Phe Ala Thr Asp Leu Phe Asn Met Leu Ser Met Asp Asp				
301	225	230	235	240	
303	tgc act aca aat acc tca gag gca act cct ggc gat act cct gcc gat				768
304	Ser Thr Thr Asn Thr Ser Glu Ala Thr Pro Gly Asp Thr Pro Ala Asp				
305	245	250	255		
307	gat aac tca tgg gct ggc ttt cag tct gct gga agt ggt caa acg gca				816
308	Asp Asn Ser Trp Ala Gly Phe Gln Ser Ala Gly Ser Gly Gln Thr Ala				

**VERIFICATION SUMMARY** DATE: 02/08/2006  
**PATENT APPLICATION:** US/10/630,518A TIME: 12:08:13

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